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RAW SEQUENCE LISTING

DATE: 05/07/2002

PATENT APPLICATION: US/10/084,018

TIME: 11:37:44

Input Set : N:\Crf3\RULE60\10084018.raw

Output Set: N:\CRF3\05072002\J084018.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Bandman, Olga
6 Hawkins, Phillip R.
7 Hillman, Jennifer L.
8 Lal, Preeti
9 Goli, Surya K.

11 (ii) TITLE OF INVENTION: NOVEL HUMAN SERINE
12 CARBOXYPEPTIDASE

14 (iii) NUMBER OF SEQUENCES: 8

16 (iv) CORRESPONDENCE ADDRESS:

17 (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
18 (B) STREET: 3174 Porter Drive
19 (C) CITY: Palo Alto
20 (D) STATE: CA
21 (E) COUNTRY: USA
22 (F) ZIP: 94304

24 (v) COMPUTER READABLE FORM:

25 (A) MEDIUM TYPE: Diskette
26 (B) COMPUTER: IBM Compatible
27 (C) OPERATING SYSTEM: DOS
28 (D) SOFTWARE: FastSEQ for Windows Version 2.0

30 (vi) CURRENT APPLICATION DATA:

C--> 31 (A) APPLICATION NUMBER: US/10/084,018
C--> 32 (B) FILING DATE: 25-Feb-2002

34 (vii) PRIOR APPLICATION DATA:

36 (A) APPLICATION NUMBER: US/09/299,689A
37 (B) FILING DATE:
39 (A) APPLICATION NUMBER: 08/828,488
40 (B) FILING DATE:

43 (viii) ATTORNEY/AGENT INFORMATION:

44 (A) NAME: Billings, Lucy J.
45 (B) REGISTRATION NUMBER: 36,749
46 (C) REFERENCE/DOCKET NUMBER: PF-0241 US

48 (ix) TELECOMMUNICATION INFORMATION:

49 (A) TELEPHONE: 415-855 0555
50 (B) TELEFAX: 415-845-4166

53 (2) INFORMATION FOR SEQ ID NO: 1:

55 (i) SEQUENCE CHARACTERISTICS:

56 (A) LENGTH: 477 amino acids
57 (B) TYPE: amino acid
58 (C) STRANDEDNESS: single
59 (D) TOPOLOGY: linear

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61      (vii) IMMEDIATE SOURCE:
62          (A) LIBRARY: MPHGN0T03
63          (B) CLONE: 443004
64      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
65 Met Val Gly Ala Met Trp Lys Val Ile Val Ser Leu Val Leu Leu Met
66 1      5      10      15
67 Pro Gly Pro Cys Asp Gly Leu Phe His Ser Leu Tyr Arg Ser Val Ser
68 20      25      30
69 Met Pro Pro Lys Gly Asp Ser Gly Gln Pro Leu Phe Leu Thr Pro Tyr
70 35      40      45
71 Ile Glu Ala Gly Lys Ile Gln Lys Gly Arg Glu Leu Ser Leu Val Gly
72 50      55      60
73 Pro Phe Pro Gly Leu Asn Met Lys Ser Tyr Ala Asp Phe Leu Thr Val
74 65      70      75      80
75 Asn Lys Thr Tyr Asn Ser Asn Leu Phe Phe Trp Phe Phe Pro Ala Gln
76 85      90      95
77 Ile Gln Pro Glu Asp Ala Pro Val Val Leu Trp Leu Gln Gly Glu Pro
78 100     105     110
79 Gly Gly Ser Ser Met Phe Gly Leu Phe Val Glu His Gly Pro Tyr Val
80 115     120     125
81 Val Thr Ser Asn Met Thr Leu Arg Asp Arg Asp Phe Pro Trp Thr Thr
82 130     135     140
83 Thr Leu Ser Met Leu Tyr Ile Asp Asn Pro Val Gly Thr Gly Phe Ser
84 145     150     155     160
85 Phe Thr Asp Asp Thr His Gly Tyr Ala Val Asn Glu Asp Asp Val Ala
86 165     170     175
87 Arg Asp Leu Tyr Ser Ala Leu Ile Gln Phe Phe Gln Ile Phe Pro Glu
88 180     185     190
89 Tyr Lys Asn Asn Asp Phe Tyr Val Thr Gly Glu Ser Tyr Ala Gly Lys
90 195     200     205
91 Tyr Val Pro Ala Ile Ala His Leu Ile His Ser Leu Asn Pro Val Arg
92 210     215     220
93 Glu Val Lys Ile Asn Leu Asn Gly Ile Ala Ile Gly Asp Gly Tyr Ser
94 225     230     235     240
95 Asp Pro Glu Ser Ile Ile Gly Gly Tyr Ala Glu Phe Leu Tyr Gln Ile
96 245     250     255
97 Gly Leu Leu Asp Glu Lys Gln Lys Lys Tyr Phe Gln Lys Gln Cys His
98 260     265     270
99 Glu Cys Ile Glu His Ile Arg Lys Gln Asn Trp Phe Glu Ala Phe Glu
100 275     280     285
101 Ile Leu Asp Lys Leu Leu Asp Gly Asp Leu Thr Ser Asp Pro Ser Tyr
102 290     295     300
103 Phe Gln Asn Val Thr Gly Cys Ser Asn Tyr Tyr Asn Phe Leu Arg Cys
104 305     310     315     320
105 Thr Glu Pro Glu Asp Gln Leu Tyr Tyr Val Lys Phe Leu Ser Leu Pro
106 325     330     335
107 Glu Val Arg Gln Ala Ile His Val Gly Asn Gln Thr Phe Asn Asp Gly
108 340     345     350
109 Thr Ile Val Glu Lys Tyr Leu Arg Glu Asp Thr Val Gln Ser Val Lys

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112          355          360          365
113 Pro Trp Leu Thr Glu Ile Met Asn Asn Tyr Lys Val Leu Ile Tyr Asn
114          370          375          380
115 Gly Gln Leu Asp Ile Ile Val Ala Ala Ala Leu Thr Glu Arg Ser Leu
116 385          390          395          400
117 Met Gly Met Asp Trp Lys Gly Ser Gln Glu Tyr Lys Lys Ala Glu Lys
118          405          410          415
119 Lys Lys Val Trp Lys Ile Phe Lys Ser Asp Ser Gly Val Ala Gly Tyr
120          420          425          430
121 Ile Arg Gln Val Gly Asp Phe His Gln Val Ile Ile Arg Gly Gly Gly
122          435          440          445
123 His Thr Leu Pro Tyr Asp Gln Pro Leu Arg Ala Phe Asp Met Ile Asn
124          450          455          460
125 Arg Phe Ile Tyr Gly Lys Gly Trp Asp Pro Tyr Val Gly
126 465          470          475
128 (2) INFORMATION FOR SEQ ID NO: 2:
130 (i) SEQUENCE CHARACTERISTICS:
131 (A) LENGTH: 1670 base pairs
132 (B) TYPE: nucleic acid
133 (C) STRANDEDNESS: single
134 (D) TOPOLOGY: linear
136 (vii) IMMEDIATE SOURCE:
137 (A) LIBRARY: MPHNOT03
138 (B) CLONE: 443004
140 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
142 AAGCGCTGCA AGGACAACCG GCTGGGGTCC TTGCGCGCCG GGCTCAGGGA GGAGCACCGA 60
143 CTGCGCGGCA CCCTGAGAGA TGGTTGGTGC CATGTGGAAG GTGATTGTTT CGCTGGTCCT 120
144 GTTGATGCCT GGCCCTGTG ATGGGCTGTT TCACTCCCTA TACAGAAGTG TTTCCATGCC 180
145 ACCTAAGGGA GACTCAGGAC AGCCATTATT TCTACCCCTT TACATTGAAG CTGGGAAGAT 240
146 CCAAAAAGGA AGAGAAITGA GTTTGGTCGG TCCTTTCCCA GGACTGAACA TGAAGAGTTA 300
147 TGCCGACTTC CTCACCTGTGA ATAAGACTTA CAACAGCAAC CTCTTCTTCT GGTTCCTCCC 360
148 AGCTCAGATA CAGCCAGAAG ATGCCCCAGT AGTTCCTCTG CTACAGGGTG AGCCGGGAGG 420
149 TTCATCCATG TTTGGACTCT TTGTGGAACA TGGGCCCTTAT GTTGTCACAA GTAACATGAC 480
150 CTTGCGTGAC AGAGACTTCC CCTGGACCAC AACGCTCTCC ATGCTTTACA TTGACAATCC 540
151 AGTGGGCACA GGCTTCAGTT TTA CTGATGA TACCCACGGA TATGCAGTCA ATGAGGACGA 600
152 TGTAGCACGG GATTTATACA GTGCACTAAT TCAGTTTTTC CAGATATTTT CTGAATATAA 660
153 AAATAATGAC TTTTATGTCA CTGGGGAGTC TTATGCAGGG AAATATGTGC CAGCCATTGC 720
154 ACACCTCATC CATTCCCTCA ACCCTGTGAG AGAGGTGAAG ATCAACCTGA ACGGAATTGC 780
155 TATTGGAGAT GGATATTCTG ATCCCGAATC AATTATAGGG GGCTATGCAG AATTCCCTGT 840
156 CCAAATIGGC TTGTTGGATG AGAAGCAAAA AAAGTACTTC CAGAAGCAGT GCCATGAATG 900
157 CATAGAACAC ATCAGGAAGC AGAACTGGTT TGAGGCCTTT GAAATACTGG ATAACTACT 960
158 AGATGGCGAC TTAACAAGTG ATCCTTCTTA CTTCAGAAAT GTTACAGGAT GTAGTAATTA 1020
159 CTATAACTTT TTGCGGTGCA CGGAACCTGA GGATCAGCTT TACTATGTGA AATTTTTGTC 1080
160 ACTCCAGAG GTGAGACAAG CCATCCACGT GGGGAATCAG ACTTTTAATG ATGGAATAT 1140
161 AGTTGAAAAG TACTTGCGAG AAGATACAGT ACAGTCAGTT AAGCCATGGT TAACTGAAAT 1200
162 CATGAATAAT TATAAGGTTT TGATCTACAA TGGCCAACTG GACATCATCG TGGCAGCTGC 1260
163 CCTGACAGAG CGTCCCTTGA TGGGCATGGA CTGGAAAGGA TCCAGGAAT ACAAGAAGGC 1320
164 AGAAAAAAA AAAGTTTGGG AGATCTTTAA ATCTGACAGT GGAGTGGCTG GTTACATCCG 1380
165 GCAAGTGGGT GACTTCCATC AGGTAATTAT TCGAGGTGGA GGACATACTT TACCCTATGA 1440

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```

166 CCAGCCTCTG AGAGCTTTTG ACATGATTAA TCGATTTCATT TATGGAAAAG GATGGGATCC 1500
167 TTATGTTGGA TAAACTACCT TCCCAAAAAGA GAACATCAGA GGTTTTTCATT GCTGAAAAGA 1560
168 AAATCGTAAA AACAGAAAAT GTCATAGGAA TAAAAAAATT ATCTTTTCAT ATCTGCAAGA 1620
169 ICTTTTTCAT CAATAAAAAT TATCCTTGAA ACAAAAAAAA AAAGAAAAAG 1670

```

171 (2) INFORMATION FOR SEQ ID NO: 3:

173 (i) SEQUENCE CHARACTERISTICS:

174 (A) LENGTH: 476 amino acids

175 (B) TYPE: amino acid

176 (C) STRANDEDNESS: single

177 (D) TOPOLOGY: linear

179 (vii) IMMEDIATE SOURCE:

180 (A) LIBRARY: MMLR3DT01

181 (B) CLONE: 566993

183 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

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185 Met Val Gly Ala Met Trp Lys Val Ile Val Ser Leu Val Leu Leu Met
186 1 5 10 15
187 Pro Gly Pro Cys Asp Gly Leu Phe His Ser Leu Tyr Arg Ser Val Ser
188 20 25 30
189 Met Pro Pro Lys Gly Asp Ser Gly Gln Pro Leu Phe Leu Thr Pro Tyr
190 35 40 45
191 Ile Glu Ala Gly Lys Ile Gln Lys Gly Arg Glu Leu Ser Leu Val Gly
192 50 55 60
193 Pro Phe Pro Gly Leu Asn Met Lys Ser Tyr Ala Gly Phe Leu Thr Val
194 65 70 75 80
195 Asn Lys Thr Tyr Asn Ser Asn Leu Phe Phe Trp Phe Phe Pro Ala Gln
196 85 90 95
197 Ile Gln Pro Glu Asp Ala Pro Val Val Leu Trp Leu Gln Gly Gly Pro
198 100 105 110
W--> 199 Gly Gly Ser Ser Met Xaa Gly Leu Phe Val Glu His Gly Pro Tyr Val
200 115 120 125
201 Val Thr Ser Asn Met Thr Leu Arg Asp Arg Asp Phe Pro Trp Thr Thr
202 130 135 140
W--> 203 Thr Xaa Ser Met Leu Tyr Ile Asp Asn Pro Val Gly Thr Gly Phe Ser
204 145 150 155 160
205 Phe Thr Asp Asp Thr His Gly Tyr Ala Val Asn Glu Asp Asp Val Ala
206 165 170 175
207 Arg Asp Leu Tyr Ser Ala Leu Ile Gln Phe Phe Gln Ile Phe Pro Glu
208 180 185 190
209 Tyr Lys Asn Asn Asp Phe Tyr Val Thr Gly Glu Ser Tyr Ala Gly Lys
210 195 200 205
211 Tyr Val Pro Ala Ile Ala His Leu Ile His Ser Leu Asn Pro Val Arg
212 210 215 220
213 Glu Val Lys Ile Asn Leu Asn Gly Ile Ala Ile Gly Asp Gly Tyr Ser
214 225 230 235 240
215 Asp Pro Glu Ser Ile Ile Gly Gly Tyr Ala Glu Phe Leu Tyr Gln Ile
216 245 250 255
217 Gly Leu Leu Asp Glu Lys Gln Lys Lys Tyr Phe Gln Lys Gln Cys His
218 260 265 270
219 Glu Cys Ile Glu His Ile Arg Lys Gln Asn Trp Phe Glu Ala Phe Glu

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```

220          275          280          285
221 Ile Leu Asp Lys Leu Leu Asp Gly Asp Leu Thr Ser Asp Pro Ser Tyr
222          290          295          300
223 Phe Gln Asn Val Thr Gly Cys Ser Asn Tyr Tyr Asn Phe Leu Arg Cys
224 305          310          315          320
225 Thr Glu Pro Glu Asp Gln Leu Tyr Tyr Val Lys Phe Leu Ser Leu Pro
226          325          330          335
227 Glu Val Arg Gln Ala Ile His Val Gly Asn Gln Thr Phe Asn Asp Gly
228          340          345          350
229 Thr Ile Val Glu Lys Tyr Leu Arg Glu Asp Thr Val Gln Ser Val Lys
230          355          360          365
231 Pro Trp Leu Thr Glu Ile Met Asn Asn Tyr Lys Val Leu Ile Tyr Asn
232          370          375          380
233 Gly Gln Leu Asp Ile Ile Val Ala Ala Ala Leu Thr Glu Arg Ser Leu
234          385          390          395          400
235 Met Gly Met Asp Trp Lys Gly Ser Gln Glu Tyr Lys Lys Ala Glu Lys
236          405          410          415
237 Lys Val Trp Lys Ile Phe Lys Ser Asp Ser Glu Val Ala Gly Tyr Ile
238          420          425          430
239 Arg Gln Val Gly Asp Phe His Gln Val Ile Ile Arg Gly Gly Gly His
240          435          440          445
241 Ile Leu Pro Tyr Asp Gln Pro Leu Arg Ala Phe Asp Met Ile Asn Arg
242          450          455          460
243 Phe Ile Tyr Gly Lys Gly Trp Asp Pro Tyr Val Gly
244          465          470          475

```

246 (2) INFORMATION FOR SEQ ID NO: 4:

248 (i) SEQUENCE CHARACTERISTICS:

249 (A) LENGTH: 1551 base pairs

250 (B) TYPE: nucleic acid

251 (C) STRANDEDNESS: single

252 (D) TOPOLOGY: linear

254 (vii) IMMEDIATE SOURCE:

255 (A) LIBRARY: MMLR3DT01

256 (B) CLONE: 566993

258 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

```

260 GAAAGCTGGT ACGCCTGCNG GTNCCGGTCC GGAATTCNCG GGTNGACCCA CGCGTCCGAN      60
261 CGACTGCGCC GCACCCTGAG AGATGGTTGG TGCCATGTGG AAGGTGATTG TITCGCTGGT      120
262 CCTGTTGATG CCTGGCCCCCT GTGATGGGCT GTTTCACCTCC CTATACAGAA GIGTTTCCAT      180
263 GCCACCTAAG GGAGACTCAG GACAGCCATT ATTTCTCACC CCTTACATTG AAGCTGGGAA      240
264 GATCCAAAAA GGAAGAGAAT TGAGTTTGGT CGGCCCTTTC CCAGGACTGA ACATGAAGAG      300
265 TTATGCCGGC TTCCTCACCG TGAATAAGAC TTACAACAGC AACCTCTTCT TCTGGTTCTT      360
266 CCCAGCTCAG ATACAGCCAG AAGATGCCCC AGTAGTTCTC TGCTACAGG GTGGGCCGGG      420
267 AGGTTCATCC ATGTTWGGAC TCTTTGTGGA ACATGGGCCT TAIGTTGTCA CAAGTAACAT      480
268 GACCTTGCGT GACAGAGACT TCCCCTGGAC CACAACGCTC TCCATGCTTT ACATTGACAA      540
269 TCCAGTGGGC ACAGGCTTCA GTTTTACTGA TGATACCCAC GGATAIGCAG TCAAIGAGGA      600
270 CGATGTAGCA CGGGATTTAT ACAGTGAAGT AATTCAGTTT TTCCAGATAT TTCTGAATA      660
271 TAAAAATAAT GACTTTTATG TCACTGGGGA GTCTTATGCA GGGAAATATG TGCCAGCCAT      720
272 TGCACACCTC ATCCATTCCC TCAACCCTGT GAGAGAGGTG AAGATCAACC TGAACGGAAT      780
273 TGCTATTGGA GATGGATATT CTGATCCCGA ATCAATTATA GGGGGCTATG CAGAAITCCT      840

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/084,018

DATE: 05/07/2002
TIME: 11:37:45

Input Set : N:\Crf3\RULE60\10084018.raw
Output Set: N:\CRF3\05072002\J084018.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; Xaa Pos.118,146

Seq#:4; N Pos. 19,23,38,44,60,1550

VERIFICATION SUMMARY

DATE: 05/07/2002

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Input Set : N:\Crf3\RULE60\10084018.raw

Output Set: N:\CRF3\05072002\J084018.raw

L:31 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:32 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]

L:199 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:112

L:203 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:144